



SEQUENCE LISTING

131
<110> Norregaard-Madsen, Mads
Ostergaard, Peter Rahbek
Christensen, Claus Bo Voge
Lassen, Soren Flensted

<120> Novel Ptoteases And Variants Thereof

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<160> 45

<170> PatentIn version 3.1

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Ser Pro His Thr Pro Val Ser Ser Asp Pro Ser Tyr Lys Ala Glu Thr
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tcg gtt act tat gac cca cac att aag agc gat caa tac ggc ttg tat 192
Ser Val Thr Tyr Asp Pro His Ile Lys Ser Asp Gln Tyr Gly Leu Tyr
-45 -40 -35

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Ala Glu Lys Lys Ser Pro Ala Lys Ala Pro Tyr Ser Ile Lys Ser Val	
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att ggt tct gat gat cgg aca agg gtc acc aac aca acc gca tat ccg	336
Ile Gly Ser Asp Asp Arg Thr Arg Val Thr Asn Thr Thr Ala Tyr Pro	
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tac aga gcg atc gtt cat att tca agc agc atc ggt tca tgc acc gga	384
Tyr Arg Ala Ile Val His Ile Ser Ser Ser Ile Gly Ser Cys Thr Gly	
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tgg atg atc ggt ccg aaa acc gtc gca aca gcc gga cac tgc atc tat	432
Trp Met Ile Gly Pro Lys Thr Val Ala Thr Ala Gly His Cys Ile Tyr	
35 40 45 50	
gac aca tca agc ggt tca ttt gcc ggt aca gcc act gtt tcg ccg gga	480
Asp Thr Ser Ser Gly Ser Phe Ala Gly Thr Ala Thr Val Ser Pro Gly	
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cgg aac ggg aca agc tat cct tac ggc tca gtt aaa tcg acg cgc tac	528
Arg Asn Gly Thr Ser Tyr Pro Tyr Gly Ser Val Lys Ser Thr Arg Tyr	
70 75 80	
ttt att ccg tca gga tgg aga agc gga aac acc aat tac gat tac gga	576
Phe Ile Pro Ser Gly Trp Arg Ser Gly Asn Thr Asn Tyr Asp Tyr Gly	
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gca atc gaa cta agc gaa ccg atc ggc aat act gtc gga tac ttc gga	624
Ala Ile Glu Leu Ser Glu Pro Ile Gly Asn Thr Val Gly Tyr Phe Gly	
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Tyr Ser Tyr Thr Thr Ser Ser Leu Val Gly Thr Thr Val Thr Ile Ser	
115 120 125 130	
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Gly Tyr Pro Gly Asp Lys Thr Ala Gly Thr Gln Trp Gln His Ser Gly	
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ccg att gcc atc tcc gaa acg tat aaa ttg cag tac gca atg gac acg	768
Pro Ile Ala Ile Ser Glu Thr Tyr Lys Leu Gln Tyr Ala Met Asp Thr	
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Tyr Gly Gly Gln Ser Gly Ser Pro Val Phe Glu Gln Ser Ser Ser Arg	
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Thr Asn Cys Ser Gly Pro Cys Ser Leu Ala Val His Thr Asn Gly Val	
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Tyr Gly Gly Ser Ser Tyr Asn Arg Gly Thr Arg Ile Thr Lys Glu Val	
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Ile Gly Ser Asp Asp Arg Thr Arg Val Thr Asn Thr Thr Ala Tyr Pro
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Tyr Arg Ala Ile Val His Ile Ser Ser Ser Ile Gly Ser Cys Thr Gly
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Trp Met Ile Gly Pro Lys Thr Val Ala Thr Ala Gly His Cys Ile Tyr
 35 40 45 50

Asp Thr Ser Ser Gly Ser Phe Ala Gly Thr Ala Thr Val Ser Pro Gly
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Arg Asn Gly Thr Ser Tyr Pro Tyr Gly Ser Val Lys Ser Thr Arg Tyr
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Phe Ile Pro Ser Gly Trp Arg Ser Gly Asn Thr Asn Tyr Asp Tyr Gly
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Ala Ile Glu Leu Ser Glu Pro Ile Gly Asn Thr Val Gly Tyr Phe Gly
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Tyr Ser Tyr Thr Thr Ser Ser Leu Val Gly Thr Thr Val Thr Ile Ser
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Gly Tyr Pro Gly Asp Lys Thr Ala Gly Thr Gln Trp Gln His Ser Gly
 135 140 145

Pro Ile Ala Ile Ser Glu Thr Tyr Lys Leu Gln Tyr Ala Met Asp Thr
 150 155 160

Tyr Gly Gly Gln Ser Gly Ser Pro Val Phe Glu Gln Ser Ser Ser Arg
 165 170 175

Thr Asn Cys Ser Gly Pro Cys Ser Leu Ala Val His Thr Asn Gly Val
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Ser	Gly	Ile	Leu	Ser	Pro	Val	Asn	Ala	Thr	Gln	Ala	Glu	Thr	Leu	Thr		
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Lys	Leu	Asn	Lys	Ile	Ser	Gln	Lys	Gln	Glu	Pro	Ser	Tyr	Lys	Leu	Asp		
				-85					-80					-75			
gaa	gaa	atg	gat	tat	gtt	cta	att	gat	ttg	gaa	aca	caa	tct	gaa	tcg	189	
Glu	Glu	Met	Asp	Tyr	Val	Leu	Ile	Asp	Leu	Glu	Thr	Gln	Ser	Glu	Ser		
			-70					-65					-60				
att	att	tcg	ata	gga	gat	aat	acc	gat	ttg	gga	gat	caa	tcg	ttt	act	237	
Ile	Ile	Ser	Ile	Gly	Asp	Asn	Thr	Asp	Leu	Gly	Asp	Gln	Ser	Phe	Thr		
		-55					-50					-45					
tct	tta	ggg	aag	gtg	gga	cat	gga	gaa	ctt	gag	aaa	att	aac	tta	gaa	285	
Ser	Leu	Gly	Lys	Val	Gly	His	Gly	Glu	Leu	Glu	Lys	Ile	Asn	Leu	Glu		
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gaa	ttt	cgt	aat	cct	aat	tta	aca	gta	gta	gac	ccg	tta	aca	cgt	aag	333	
Glu	Phe	Arg	Asn	Pro	Asn	Leu	Thr	Val	Val	Asp	Pro	Leu	Thr	Arg	Lys		
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cct	att	gaa	caa	aaa	atc	agc	cct	ttt	gtt	gtt	ata	ggc	gat	gat	ggg	381	
Pro	Ile	Glu	Gln	Lys	Ile	Ser	Pro	Phe	Val	Val	Ile	Gly	Asp	Asp	Gly		
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aga	aga	caa	gtt	caa	aat	act	tct	ttc	atg	cca	ttt	cgt	gca	ctt	act	429	
Arg	Arg	Gln	Val	Gln	Asn	Thr	Ser	Phe	Met	Pro	Phe	Arg	Ala	Leu	Thr		
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tat	att	gag	ttt	gga	aac	ctt	aca	agt	aca	tgg	agt	tgt	tct	gga	ggg	477	
Tyr	Ile	Glu	Phe	Gly	Asn	Leu	Thr	Ser	Thr	Trp	Ser	Cys	Ser	Gly	Gly		
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gtg	att	gga	aca	gat	tta	gtt	gtt	act	aat	gca	cat	tgt	gta	gaa	ggg	525	
Val	Ile	Gly	Thr	Asp	Leu	Val	Val	Thr	Asn	Ala	His	Cys	Val	Glu	Gly		
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tct	gtg	tta	gca	ggg	act	gta	gtt	cct	ggg	atg	aac	aat	agt	cag	tgg	573	
Ser	Val	Leu	Ala	Gly	Thr	Val	Val	Pro	Gly	Met	Asn	Asn	Ser	Gln	Trp		
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gca	tat	ggg	cat	tat	agg	gtt	act	cag	att	atc	tac	cct	gat	caa	tac	621	
Ala	Tyr	Gly	His	Tyr	Arg	Val	Thr	Gln	Ile	Ile	Tyr	Pro	Asp	Gln	Tyr		
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aga	aat	aac	ggg	gct	tca	gag	ttt	gat	tat	gct	ata	ctt	aga	gta	gca	669	
Arg	Asn	Asn	Gly	Ala	Ser	Glu	Phe	Asp	Tyr	Ala	Ile	Leu	Arg	Val	Ala		
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cct	gac	tct	gat	gga	cgt	cat	att	gga	aac	aga	gct	gga	att	tta	tct	717	
Pro	Asp	Ser	Asp	Gly	Arg	His	Ile	Gly	Asn	Arg	Ala	Gly	Ile	Leu	Ser		
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Phe	Thr	Glu	Thr	Gly	Thr	Val	Asn	Glu	Asn	Thr	Phe	Leu	Arg	Thr	Tyr		

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Gly Tyr Pro Gly Asp Lys Ile Ser Glu Thr Lys Leu Ile Ser Leu Trp				
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gga atg gtt ggt cga tct gat gca ttt ttg cat cga gac cta ctg ttc				861
Gly Met Val Gly Arg Ser Asp Ala Phe Leu His Arg Asp Leu Leu Phe				
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Tyr Asn Met Asp Thr Tyr Phe Gly Gln Ser Gly Ser Pro Val Leu Asn				
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agc gta gat tca atg gtt gcg gtt cat aat gca ggg tat atc gtt ggt				957
Ser Val Asp Ser Met Val Ala Val His Asn Ala Gly Tyr Ile Val Gly				
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ggt aat agg gaa att aat ggt ggt cct aaa atc aga aga gat ttt aca				1005
Gly Asn Arg Glu Ile Asn Gly Gly Pro Lys Ile Arg Arg Asp Phe Thr				
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Lys Leu Asn Lys Ile Ser Gln Lys Gln Glu Pro Ser Tyr Lys Leu Asp	
	-85 -80 -75
Glu Glu Met Asp Tyr Val Leu Ile Asp Leu Glu Thr Gln Ser Glu Ser	
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Ile Ile Ser Ile Gly Asp Asn Thr Asp Leu Gly Asp Gln Ser Phe Thr	
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Ser Leu Gly Lys Val Gly His Gly Glu Leu Glu Lys Ile Asn Leu Glu	
	-40 -35 -30
Glu Phe Arg Asn Pro Asn Leu Thr Val Val Asp Pro Leu Thr Arg Lys	
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Val Ile Gly Thr Asp Leu Val Val Thr Asn Ala His Cys Val Glu Gly
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Ser Val Leu Ala Gly Thr Val Val Pro Gly Met Asn Asn Ser Gln Trp
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Ala Tyr Gly His Tyr Arg Val Thr Gln Ile Ile Tyr Pro Asp Gln Tyr
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Arg Asn Asn Gly Ala Ser Glu Phe Asp Tyr Ala Ile Leu Arg Val Ala
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Pro Asp Ser Asp Gly Arg His Ile Gly Asn Arg Ala Gly Ile Leu Ser
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Phe Thr Glu Thr Gly Thr Val Asn Glu Asn Thr Phe Leu Arg Thr Tyr
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Gly Tyr Pro Gly Asp Lys Ile Ser Glu Thr Lys Leu Ile Ser Leu Trp
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Gly Met Val Gly Arg Ser Asp Ala Phe Leu His Arg Asp Leu Leu Phe
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Tyr Asn Met Asp Thr Tyr Phe Gly Gln Ser Gly Ser Pro Val Leu Asn
 170 175 180

Ser Val Asp Ser Met Val Ala Val His Asn Ala Gly Tyr Ile Val Gly
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Ile Ser Ile Phe Ser Ser Gly Ile Tyr Ser Ala Gln Ala Ala Ser Ser	
-75 -70 -65	
ccg cat acc cca gtc tcc agc gac cct tcg tac aag ccc ggc tcc acc	144
Pro His Thr Pro Val Ser Ser Asp Pro Ser Tyr Lys Pro Gly Ser Thr	
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Tyr Asp Pro Asn Ile Lys Ile Asp Asn Asn Gly Ala Tyr Ser Lys Ala	
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Phe Glu Gly Thr Gly Thr Pro Gly Gly Ser Val Gln Ala Lys Pro Lys	
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aaa gaa tcg ccc gcc ggc ccg cct tac agc cct aaa tcg gta atc ggc	288
Lys Glu Ser Pro Ala Gly Pro Tyr Ser Pro Lys Ser Val Ile Gly	
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Ser Asp Glu Arg Thr Arg Val Thr Asp Thr Thr Ala Phe Pro Tyr Arg	
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gca atc gtc cat att tca agc agc atc ggc tca tgc aca ggc tgg ctg	384
Ala Ile Val His Ile Ser Ser Ser Ile Gly Ser Cys Thr Gly Trp Leu	
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ggt tca gct tac cct tac gga tct gtt aca tgc acc cgc tat ttc atc Gly Ser Ala Tyr Pro Tyr Gly Ser Val Thr Ser Thr Arg Tyr Phe Ile 70 75 80	528
ccg tgc ggt tgg cag agc gga aat tcc aat tat gac tac gca gcg atc Pro Ser Gly Trp Gln Ser Gly Asn Ser Asn Tyr Asp Tyr Ala Ala Ile 85 90 95 100	576
gag ctc agc cag ccg atc ggc aat acc gtc gga tat ttc gga tat tca Glu Leu Ser Gln Pro Ile Gly Asn Thr Val Gly Tyr Phe Gly Tyr Ser 105 110 115	624
tac acc gct tca tgc ctt gca gga gca ggc gtg acc atc agc gga tat Tyr Thr Ala Ser Ser Leu Ala Gly Ala Gly Val Thr Ile Ser Gly Tyr 120 125 130	672
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 -10 -5 -1 1

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Ile Gly Pro Lys Thr Val Ala Thr Ala Gly His Cys Val Tyr Asp Thr
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Ala Ser Arg Ser Phe Ala Gly Thr Ala Thr Val Ser Pro Gly Arg Asn
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Gly Ser Ala Tyr Pro Tyr Gly Ser Val Thr Ser Thr Arg Tyr Phe Ile
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Pro Ser Gly Trp Gln Ser Gly Asn Ser Asn Tyr Asp Tyr Ala Ala Ile
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Tyr Thr Ala Ser Ser Leu Ala Gly Ala Gly Val Thr Ile Ser Gly Tyr
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Pro Gly Asp Lys Thr Thr Gly Thr Gln Trp Gln Met Ser Gly Thr Ile
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Ala Val Ser Glu Thr Tyr Lys Leu Gln Tyr Ala Ile Asp Thr Tyr Gly
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Gly Gln Ser Gly Ser Pro Val Tyr Glu Lys Ser Ser Ser Arg Thr Asn

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75 80 85	
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125 130 135	
atg aga tca act ggc aag atc tcg cag tgg gag atg tca ggt cct gtg Met Arg Ser Thr Gly Lys Ile Ser Gln Trp Glu Met Ser Gly Pro Val	720
140 145 150	
aca aga gaa gat acg aat ctc gca tac tat atg att gat aca ttt agt Thr Arg Glu Asp Thr Asn Leu Ala Tyr Tyr Met Ile Asp Thr Phe Ser	768
155 160 165	
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170 175 180	
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185 190 195 200	
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Thr Ser Asp Tyr Asp Met Val Thr Ser Asp Gly Lys Val Ile Ser Ser
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Ser Asp Phe His Asn Asp Thr Lys Ser Pro Ser Ser Phe Asp Lys Val
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Asp Asp Leu Ser Ser Thr Val Gly Glu Lys Val Lys Pro Leu Ser Lys
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Tyr Leu Lys Asp Phe Gln Thr Lys Val Val Ile Gly Asp Asp Gly Arg
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Thr Lys Val Ala Asn Thr Arg Val Ala Pro Tyr Asn Ser Ile Ala Tyr
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Thr Thr Phe Gly Gly Ser Ser Cys Thr Gly Thr Leu Ile Ala Pro Asn
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Lys Ile Leu Thr Asn Gly His Cys Val Tyr Asn Thr Ala Ser Arg Ser
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Tyr Ser Ala Lys Gly Ser Val Tyr Pro Gly Met Asn Asp Ser Thr Ala
 60 65 70

Val Asn Gly Ser Ala Asn Met Thr Glu Phe Tyr Val Pro Ser Gly Tyr
 75 80 85

Ile Asn Thr Gly Ala Ser Gln Tyr Asp Phe Ala Val Ile Lys Thr Asp
 90 95 100

Thr Asn Ile Gly Asn Thr Val Gly Tyr Arg Ser Ile Arg Gln Val Thr
 105 110 115 120

Asn Leu Thr Gly Thr Thr Ile Lys Ile Ser Gly Tyr Pro Gly Asp Lys
 125 130 135

Met Arg Ser Thr Gly Lys Ile Ser Gln Trp Glu Met Ser Gly Pro Val
140 145 150

Thr Arg Glu Asp Thr Asn Leu Ala Tyr Tyr Met Ile Asp Thr Phe Ser
155 160 165

Gly Asn Ser Gly Ser Ala Met Leu Asp Gln Asn Gln Gln Ile Val Gly
170 175 180

Val His Asn Ala Gly Tyr Ser Asn Gly Thr Ile Asn Gly Gly Pro Lys
185 190 195 200

Ala Thr Ala Ala Phe Val Glu Phe Ile Asn Tyr Ala Lys Ala Gln
205 210 215

<210> 9
<211> 954
<212> DNA
<213> Bacillus

<220>
<221> CDS
<222> (1)..(954)
<223>

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<221> mat_peptide
<222> (289)..()
<223>

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<221> sig_peptide
<222> (1)..(84)
<223>

<220>
<221> pro-peptide
<222> (85)..(288)
<223>

<400> 9
atg aaa aaa agt gtg aca cgc gta tta atg gcc ggt ctt att gga ata 48
Met Lys Lys Ser Val Thr Arg Val Leu Met Ala Gly Leu Ile Gly Ile
-95 -90 -85
tct att tat tct atg ggc atc gac tcc gct caa gct gca tca tcg ccg 96
Ser Ile Tyr Ser Met Gly Ile Asp Ser Ala Gln Ala Ala Ser Ser Pro
-80 -75 -70 -65
cat act cct gtc tct agc gat cct tca tac aag ccc gac tca tcc gca 144

His Thr Pro Val Ser Ser Asp Pro Ser Tyr Lys Pro Asp Ser Ser Ala	
-60 -55 -50	
agc tat gat cct gct att aaa acc aac aaa aac ggc gcc tat tca aaa	192
Ser Tyr Asp Pro Ala Ile Lys Thr Asn Lys Asn Gly Ala Tyr Ser Lys	
-45 -40 -35	
gca ttt gaa ggt aca gga aaa cta gac gct ccc ctt tat cag gaa aaa	240
Ala Phe Glu Gly Thr Gly Lys Leu Asp Ala Pro Leu Tyr Gln Glu Lys	
-30 -25 -20	
agc aaa cca acc aaa aaa tcc cct gcc gga cca cgt tac agc ccc aaa	288
Ser Lys Pro Thr Lys Lys Ser Pro Ala Gly Pro Arg Tyr Ser Pro Lys	
-15 -10 -5 -1	
tcc gtg att ggt tct gat gaa cgg acg aga gtg aca aac act acc gca	336
Ser Val Ile Gly Ser Asp Glu Arg Thr Arg Val Thr Asn Thr Thr Ala	
1 5 10 15	
tat cca tac aga gcg atc gtg cat att tca agc agc atc ggg tct tgc	384
Tyr Pro Tyr Arg Ala Ile Val His Ile Ser Ser Ser Ile Gly Ser Cys	
20 25 30	
acc ggc tcc ctg atc ggt ccg aaa acg gtg gca acg gcc gga cac tgc	432
Thr Gly Ser Leu Ile Gly Pro Lys Thr Val Ala Thr Ala Gly His Cys	
35 40 45	
att tat gac aca gcg agc ggg tca ttc gcc gga acc gct acc gtt tct	480
Ile Tyr Asp Thr Ala Ser Gly Ser Phe Ala Gly Thr Ala Thr Val Ser	
50 55 60	
ccg gga cgg aac ggt tca aca tat ccg tac gga tca gtt aca tca acc	528
Pro Gly Arg Asn Gly Ser Thr Tyr Pro Tyr Gly Ser Val Thr Ser Thr	
65 70 75 80	
cgc tat ttc atc ccg tca ggc tat cga agc gga aat tcg aat tac gac	576
Arg Tyr Phe Ile Pro Ser Gly Tyr Arg Ser Gly Asn Ser Asn Tyr Asp	
85 90 95	
tac gga gcc ata gag ctc agc cag ccg atc ggc aac acc gtc ggg tat	624
Tyr Gly Ala Ile Glu Leu Ser Gln Pro Ile Gly Asn Thr Val Gly Tyr	
100 105 110	
ttc gga tat tcc tac acc acc tcg tct ctc gtt ggg tca agc gtt acc	672
Phe Gly Tyr Ser Tyr Thr Thr Ser Ser Leu Val Gly Ser Val Thr	
115 120 125	
atc atc gga tat cca ggc gac aaa aca tcg ggc acc caa tgg cag atg	720
Ile Ile Gly Tyr Pro Gly Asp Lys Thr Ser Gly Thr Gln Trp Gln Met	
130 135 140	
tcc gga aat atc gcc gtc tca gaa aca tat aaa ctg caa tat gcg atc	768
Ser Gly Asn Ile Ala Val Ser Glu Thr Tyr Lys Leu Gln Tyr Ala Ile	
145 150 155 160	
gac aca tac gga ggg cag agc ggc tct ccc gta tat gag gcg agc agc	816
Asp Thr Tyr Gly Gly Gln Ser Gly Ser Pro Val Tyr Glu Ala Ser Ser	
165 170 175	
tcc aga acg aat tgc agc ggc cca tgt tcg ctg gcc gtt cat acg aat	864
Ser Arg Thr Asn Cys Ser Gly Pro Cys Ser Leu Ala Val His Thr Asn	

	180		185		190	
	ggg gtg tac gga gga tct tca tac aac aga ggc acc cgg att aca aaa					912
	Gly Val Tyr Gly Gly Ser Ser Tyr Asn Arg Gly Thr Arg Ile Thr Lys					
	195		200		205	
	gaa gta ttc gat aat ttg aca aac tgg aaa aac agc gcc caa					954
	Glu Val Phe Asp Asn Leu Thr Asn Trp Lys Asn Ser Ala Gln					
	210		215		220	
<210>	10					
<211>	318					
<212>	PRT					
<213>	Bacillus					
<400>	10					
Met	Lys Lys Ser Val Thr Arg Val Leu Met Ala Gly Leu Ile Gly Ile					
	-95		-90		-85	
Ser	Ile Tyr Ser Met Gly Ile Asp Ser Ala Gln Ala Ala Ser Ser Pro					
	-80		-75		-70	-65
His	Thr Pro Val Ser Ser Asp Pro Ser Tyr Lys Pro Asp Ser Ser Ala					
		-60		-55		-50
Ser	Tyr Asp Pro Ala Ile Lys Thr Asn Lys Asn Gly Ala Tyr Ser Lys					
		-45		-40		-35
Ala	Phe Glu Gly Thr Gly Lys Leu Asp Ala Pro Leu Tyr Gln Glu Lys					
		-30		-25		-20
Ser	Lys Pro Thr Lys Lys Ser Pro Ala Gly Pro Arg Tyr Ser Pro Lys					
		-15		-10		-5
						-1
Ser	Val Ile Gly Ser Asp Glu Arg Thr Arg Val Thr Asn Thr Thr Ala					
1		5		10		15
Tyr	Pro Tyr Arg Ala Ile Val His Ile Ser Ser Ser Ile Gly Ser Cys					
		20		25		30
Thr	Gly Ser Leu Ile Gly Pro Lys Thr Val Ala Thr Ala Gly His Cys					
		35		40		45
Ile	Tyr Asp Thr Ala Ser Gly Ser Phe Ala Gly Thr Ala Thr Val Ser					
		50		55		60
Pro	Gly Arg Asn Gly Ser Thr Tyr Pro Tyr Gly Ser Val Thr Ser Thr					
65			70		75	80

Arg Tyr Phe Ile Pro Ser Gly Tyr Arg Ser Gly Asn Ser Asn Tyr Asp
 85 90 95
 Tyr Gly Ala Ile Glu Leu Ser Gln Pro Ile Gly Asn Thr Val Gly Tyr
 100 105 110
 Phe Gly Tyr Ser Tyr Thr Thr Ser Ser Leu Val Gly Ser Ser Val Thr
 115 120 125
 Ile Ile Gly Tyr Pro Gly Asp Lys Thr Ser Gly Thr Gln Trp Gln Met
 130 135 140
 Ser Gly Asn Ile Ala Val Ser Glu Thr Tyr Lys Leu Gln Tyr Ala Ile
 145 150 155 160
 Asp Thr Tyr Gly Gly Gln Ser Gly Ser Pro Val Tyr Glu Ala Ser Ser
 165 170 175
 Ser Arg Thr Asn Cys Ser Gly Pro Cys Ser Leu Ala Val His Thr Asn
 180 185 190
 Gly Val Tyr Gly Gly Ser Ser Tyr Asn Arg Gly Thr Arg Ile Thr Lys
 195 200 205
 Glu Val Phe Asp Asn Leu Thr Asn Trp Lys Asn Ser Ala Gln
 210 215 220

<210> 11
 <211> 906
 <212> DNA
 <213> Bacillus

<220>
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 <222> (1)..(906)
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<220>
 <221> mat_peptide
 <222> (262)..()
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<220>
 <221> sig_peptide
 <222> (1)..(75)
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<220>

<221> pro-peptide
 <222> (76)..(261)
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<400> 11
 atg aaa aag gtg aaa aaa tta atc cct tct cta ctc gtt ttt ggt gct 48
 Met Lys Lys Val Lys Lys Leu Ile Pro Ser Leu Leu Val Phe Gly Ala
 -85 -80 -75

tta agt gtg cct agt ttt gcc cat gca gca tct gat tca gta ctt acg 96
 Leu Ser Val Pro Ser Phe Ala His Ala Ala Ser Asp Ser Val Leu Thr
 -70 -65 -60

tct gat tat gac atg gtg act tct gac gga aag gtg att tct tca gct 144
 Ser Asp Tyr Asp Met Val Thr Ser Asp Gly Lys Val Ile Ser Ser Ala
 -55 -50 -45 -40

gac ttc cac aac gat atg aaa acc ccc tca tcc ttt gac aaa gtg gat 192
 Asp Phe His Asn Asp Met Lys Thr Pro Ser Ser Phe Asp Lys Val Asp
 -35 -30 -25

gat ctc tct tct act att ggc gaa aaa gta aaa cca ctc aca aca tat 240
 Asp Leu Ser Ser Thr Ile Gly Glu Lys Val Lys Pro Leu Thr Thr Tyr
 -20 -15 -10

tta aaa gac ttt caa aca aaa gta gtc att gga gac gat ggt aga aca 288
 Leu Lys Asp Phe Gln Thr Lys Val Val Ile Gly Asp Asp Gly Arg Thr
 -5 -1 1 5

aaa gtg acg aat aca aga gta gca ccc tat aat tct att gct tat att 336
 Lys Val Thr Asn Thr Arg Val Ala Pro Tyr Asn Ser Ile Ala Tyr Ile
 10 15 20 25

aca ttt ggt gga tct agc tgc act gga aca ctc att gct cca aac aaa 384
 Thr Phe Gly Gly Ser Ser Cys Thr Gly Thr Leu Ile Ala Pro Asn Lys
 30 35 40

ata ttg aca aac gga cac tgc gtc tac aat aca gcc aca aga agt tat 432
 Ile Leu Thr Asn Gly His Cys Val Tyr Asn Thr Ala Thr Arg Ser Tyr
 45 50 55

agt gca aaa ggg tct gtc tac cca ggc atg aat gac agc acg gct gtg 480
 Ser Ala Lys Gly Ser Val Tyr Pro Gly Met Asn Asp Ser Thr Ala Val
 60 65 70

aac ggc tca gca aac atg acc gaa ttc tat gta cca agc gga tat atc 528
 Asn Gly Ser Ala Asn Met Thr Glu Phe Tyr Val Pro Ser Gly Tyr Ile
 75 80 85

aac acg ggg gcg agt caa tat gat ttt gcc gtc att aaa aca gat acg 576
 Asn Thr Gly Ala Ser Gln Tyr Asp Phe Ala Val Ile Lys Thr Asp Thr
 90 95 100 105

aac att gga aat acg gtc ggc tat cgc tct att cgt caa gtg aca aat 624
 Asn Ile Gly Asn Thr Val Gly Tyr Arg Ser Ile Arg Gln Val Thr Asn
 110 115 120

cta aca ggt aca acg att aaa att tct gga tat cca ggt gat aaa atg 672
 Leu Thr Gly Thr Thr Ile Lys Ile Ser Gly Tyr Pro Gly Asp Lys Met
 125 130 135

aga tcg act ggc aaa gtg tca caa tgg gaa atg tca ggt cca gtc acg 720
 Arg Ser Thr Gly Lys Val Ser Gln Trp Glu Met Ser Gly Pro Val Thr
 140 145 150

aga gaa gat acg aat ctc gca tac tat acg atc gat aca ttt agc gga 768
 Arg Glu Asp Thr Asn Leu Ala Tyr Tyr Thr Ile Asp Thr Phe Ser Gly
 155 160 165

aac tct ggc tct gcg atg cta gat cag aac caa caa atc gtc ggg gtc 816
 Asn Ser Gly Ser Ala Met Leu Asp Gln Asn Gln Gln Ile Val Gly Val
 170 175 180 185

cat aat gcg ggt tat tca aat gga acg atc aac ggt gga cca aaa gcg 864
 His Asn Ala Gly Tyr Ser Asn Gly Thr Ile Asn Gly Gly Pro Lys Ala
 190 195 200

act gct gcc ttt gtt gaa ttt atc aac tat gcg aag gcg caa 906
 Thr Ala Ala Phe Val Glu Phe Ile Asn Tyr Ala Lys Ala Gln
 205 210 215

<210> 12
 <211> 302
 <212> PRT
 <213> Bacillus

<400> 12

Met Lys Lys Val Lys Lys Leu Ile Pro Ser Leu Leu Val Phe Gly Ala
 -85 -80 -75

Leu Ser Val Pro Ser Phe Ala His Ala Ala Ser Asp Ser Val Leu Thr
 -70 -65 -60

Ser Asp Tyr Asp Met Val Thr Ser Asp Gly Lys Val Ile Ser Ser Ala
 -55 -50 -45 -40

Asp Phe His Asn Asp Met Lys Thr Pro Ser Ser Phe Asp Lys Val Asp
 -35 -30 -25

Asp Leu Ser Ser Thr Ile Gly Glu Lys Val Lys Pro Leu Thr Thr Tyr
 -20 -15 -10

Leu Lys Asp Phe Gln Thr Lys Val Val Ile Gly Asp Asp Gly Arg Thr
 -5 -1 1 5

Lys Val Thr Asn Thr Arg Val Ala Pro Tyr Asn Ser Ile Ala Tyr Ile
 10 15 20 25

Thr Phe Gly Gly Ser Ser Cys Thr Gly Thr Leu Ile Ala Pro Asn Lys
 30 35 40

Ile Leu Thr Asn Gly His Cys Val Tyr Asn Thr Ala Thr Arg Ser Tyr
45 50 55

Ser Ala Lys Gly Ser Val Tyr Pro Gly Met Asn Asp Ser Thr Ala Val
60 65 70

Asn Gly Ser Ala Asn Met Thr Glu Phe Tyr Val Pro Ser Gly Tyr Ile
75 80 85

Asn Thr Gly Ala Ser Gln Tyr Asp Phe Ala Val Ile Lys Thr Asp Thr
90 95 100 105

Asn Ile Gly Asn Thr Val Gly Tyr Arg Ser Ile Arg Gln Val Thr Asn
110 115 120

Leu Thr Gly Thr Thr Ile Lys Ile Ser Gly Tyr Pro Gly Asp Lys Met
125 130 135

Arg Ser Thr Gly Lys Val Ser Gln Trp Glu Met Ser Gly Pro Val Thr
140 145 150

Arg Glu Asp Thr Asn Leu Ala Tyr Tyr Thr Ile Asp Thr Phe Ser Gly
155 160 165

Asn Ser Gly Ser Ala Met Leu Asp Gln Asn Gln Gln Ile Val Gly Val
170 175 180 185

His Asn Ala Gly Tyr Ser Asn Gly Thr Ile Asn Gly Gly Pro Lys Ala
190 195 200

Thr Ala Ala Phe Val Glu Phe Ile Asn Tyr Ala Lys Ala Gln
205 210 215

<210> 13
<211> 939
<212> DNA
<213> Bacillus

<220>
<221> CDS
<222> (1)..(939)
<223>

<220>
<221> mat_peptide
<222> (280)..()
<223>

<220>
 <221> pro-peptide
 <222> (103)..(279)
 <223>

<400> 13

atg aaa tta gtt cca aga ttc aga aaa caa tgg ttc gct tac tta acg	48
Met Lys Leu Val Pro Arg Phe Arg Lys Gln Trp Phe Ala Tyr Leu Thr	
-90 -85 -80	
gtt ttg tgt ttg gct ttg gca gca gcg gtt tct ttt ggc gta ccg gca	96
Val Leu Cys Leu Ala Leu Ala Ala Val Ser Phe Gly Val Pro Ala	
-75 -70 -65	
aaa gcg gca gag aac ccg caa act tct gta tcg aat acc ggt aaa gaa	144
Lys Ala Ala Glu Asn Pro Gln Thr Ser Val Ser Asn Thr Gly Lys Glu	
-60 -55 -50	
gct gat gct acg aaa aac caa acg tca aaa gca gat cag gtt tcc gcc	192
Ala Asp Ala Thr Lys Asn Gln Thr Ser Lys Ala Asp Gln Val Ser Ala	
-45 -40 -35 -30	
cct tat gag gga acc gga aaa aca agt aaa tcg tta tac ggc ggc caa	240
Pro Tyr Glu Gly Thr Gly Lys Thr Ser Lys Ser Leu Tyr Gly Gly Gln	
-25 -20 -15	
acg gaa ctg gaa aaa aac att caa acc tta cag cct tcg agc att atc	288
Thr Glu Leu Glu Lys Asn Ile Gln Thr Leu Gln Pro Ser Ser Ile Ile	
-10 -5 -1 1	
gga act gat gaa cgc acc aga atc tcc agc acg aca tct ttt cca tat	336
Gly Thr Asp Glu Arg Thr Arg Ile Ser Ser Thr Thr Ser Phe Pro Tyr	
5 10 15	
aga gca acc gtt caa ctg tca atc aag tat ccc aac act tca agc act	384
Arg Ala Thr Val Gln Leu Ser Ile Lys Tyr Pro Asn Thr Ser Ser Thr	
20 25 30 35	
tat gga tgt acc gga ttt tta gtc aat cca aat aca gtc gtc acg gct	432
Tyr Gly Cys Thr Gly Phe Leu Val Asn Pro Asn Thr Val Val Thr Ala	
40 45 50	
gga cat tgt gtg tac agc cag gat cat gga tgg gct tcg acg ata acc	480
Gly His Cys Val Tyr Ser Gln Asp His Gly Trp Ala Ser Thr Ile Thr	
55 60 65	
gcc gcg ccg ggc cgc aat ggt tcg tca tat ccg tac ggt act tat tca	528
Ala Ala Pro Gly Arg Asn Gly Ser Ser Tyr Pro Tyr Gly Thr Tyr Ser	
70 75 80	
ggc acg atg ttt tac tcc gtc aaa gga tgg acg gaa agc aaa gac acc	576
Gly Thr Met Phe Tyr Ser Val Lys Gly Trp Thr Glu Ser Lys Asp Thr	
85 90 95	
aac tat gat tac gga gct att aaa tta aac ggt tct cct gga aac acg	624
Asn Tyr Asp Tyr Gly Ala Ile Lys Leu Asn Gly Ser Pro Gly Asn Thr	
100 105 110 115	
gtt ggc tgg tac ggc tac cgg act aca aac agc agc agt ccc gtg ggc	672
Val Gly Trp Tyr Gly Tyr Arg Thr Thr Asn Ser Ser Ser Pro Val Gly	

	120	125	130	
ctt tcc tcg tca gtg aca gga ttc cca tgt gac aaa acc ttt ggc acg				720
Leu Ser Ser Ser Val Thr Gly Phe Pro Cys Asp Lys Thr Phe Gly Thr				
	135	140	145	
atg tgg tct gat aca aag ccg att cgc tcc gct gaa acg tat aag ctg				768
Met Trp Ser Asp Thr Lys Pro Ile Arg Ser Ala Glu Thr Tyr Lys Leu				
	150	155	160	
acc tat aca acc gat acg tac ggc tgc caa agc ggc tcg cct gtt tat				816
Thr Tyr Thr Thr Asp Thr Tyr Gly Cys Gln Ser Gly Ser Pro Val Tyr				
	165	170	175	
cga aac tac agt gat aca ggg cag aca gct att gcc att cac acg aac				864
Arg Asn Tyr Ser Asp Thr Gly Gln Thr Ala Ile Ala Ile His Thr Asn				
	180	185	190	195
gga gga tcg tca tat aac ttg gga aca agg gtg acg aac gat gta ttc				912
Gly Gly Ser Ser Tyr Asn Leu Gly Thr Arg Val Thr Asn Asp Val Phe				
	200	205	210	
aac aat att caa tat tgg gca aat caa				939
Asn Asn Ile Gln Tyr Trp Ala Asn Gln				
	215	220		

<210> 14
 <211> 313
 <212> PRT
 <213> Bacillus

<400> 14

Met Lys Leu Val Pro Arg Phe Arg Lys Gln Trp Phe Ala Tyr Leu Thr	
	-90 -85 -80

Val Leu Cys Leu Ala Leu Ala Ala Ala Val Ser Phe Gly Val Pro Ala	
	-75 -70 -65

Lys Ala Ala Glu Asn Pro Gln Thr Ser Val Ser Asn Thr Gly Lys Glu	
	-60 -55 -50

Ala Asp Ala Thr Lys Asn Gln Thr Ser Lys Ala Asp Gln Val Ser Ala	
	-45 -40 -35 -30

Pro Tyr Glu Gly Thr Gly Lys Thr Ser Lys Ser Leu Tyr Gly Gly Gln	
	-25 -20 -15

Thr Glu Leu Glu Lys Asn Ile Gln Thr Leu Gln Pro Ser Ser Ile Ile	
	-10 -5 -1 1

Gly Thr Asp Glu Arg Thr Arg Ile Ser Ser Thr Thr Ser Phe Pro Tyr	
	5 10 15

Arg Ala Thr Val Gln Leu Ser Ile Lys Tyr Pro Asn Thr Ser Ser Thr
20 25 30 35

Tyr Gly Cys Thr Gly Phe Leu Val Asn Pro Asn Thr Val Val Thr Ala
40 45 50

Gly His Cys Val Tyr Ser Gln Asp His Gly Trp Ala Ser Thr Ile Thr
55 60 65

Ala Ala Pro Gly Arg Asn Gly Ser Ser Tyr Pro Tyr Gly Thr Tyr Ser
70 75 80

Gly Thr Met Phe Tyr Ser Val Lys Gly Trp Thr Glu Ser Lys Asp Thr
85 90 95

Asn Tyr Asp Tyr Gly Ala Ile Lys Leu Asn Gly Ser Pro Gly Asn Thr
100 105 110 115

Val Gly Trp Tyr Gly Tyr Arg Thr Thr Asn Ser Ser Ser Pro Val Gly
120 125 130

Leu Ser Ser Ser Val Thr Gly Phe Pro Cys Asp Lys Thr Phe Gly Thr
135 140 145

Met Trp Ser Asp Thr Lys Pro Ile Arg Ser Ala Glu Thr Tyr Lys Leu
150 155 160

Thr Tyr Thr Thr Asp Thr Tyr Gly Cys Gln Ser Gly Ser Pro Val Tyr
165 170 175

Arg Asn Tyr Ser Asp Thr Gly Gln Thr Ala Ile Ala Ile His Thr Asn
180 185 190 195

Gly Gly Ser Ser Tyr Asn Leu Gly Thr Arg Val Thr Asn Asp Val Phe
200 205 210

Asn Asn Ile Gln Tyr Trp Ala Asn Gln
215 220

<210> 15

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 15

Glu Lys Ala Ser
1

<210> 16

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 16

Ser Glu Lys Ala Ser Thr
1 5

<210> 17

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 17

Ser Glu Glu Thr
1

<210> 18

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<220>

<221> misc_feature

<222> (21)..(21)

<223> n denotes a, g, c, or t

<220>

<221> misc_feature

<222> (36)..(36)

<223> n denotes a, g, c, or t

<400> 18

ggatggagaa gcggaacac naaytaygay tayggngc

38

<210> 19

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 19

Gly Trp Arg Ser Gly Asn Tyr Asp Tyr Gly
1 5 10

<210> 20

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<220>

<221> misc_feature

<222> (12)..(12)

<223> n denotes deoxyInosine

<220>

<221> misc_feature

<222> (15)..(15)

<223> n denotes deoxyinosine

<220>

<221> misc_feature

<222> (18)..(18)

<223> n denotes a, g, c, or t

<220>

<221> misc_feature

<222> (21)..(21)

<223> n denotes a, g, c, or t

<220>

<221> misc_feature

<222> (24)..(24)

<223> n denotes a, g, c, or t

<400> 20

cccaagcttg tngynacngc nggncayt

28

<210> 21

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<220>
 <221> misc_feature
 <222> (2)..(2)
 <223> Xaa denotes Ala or Val

<400> 21

Val Xaa Thr Ala Gly His
 1 5

<210> 22
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<220>
 <221> misc_feature
 <222> (22)..(22)
 <223> n denotes a, g, c, or t

<220>
 <221> misc_feature
 <222> (25)..(25)
 <223> n denotes a, g, c, or t

<220>
 <221> misc_feature
 <222> (31)..(31)
 <223> n denotes a, g, c, or t

<400> 22
 gaataccggt gaaccgcttt gncmncrta ngtrtc

36

<210> 23
 <211> 12
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <221> misc_feature
 <222> (5)..(5)
 <223> Xaa denotes Gly or Cys or Trp

<400> 23

Asp Thr Tyr Gly Xaa Gln Ser Gly Ser Pro Val Phe
 1 5 10

<210> 24
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<220>
<221> misc_feature
<222> (15)..(15)
<223> n denotes a, g, c, or t

<220>
<221> misc_feature
<222> (18)..(18)
<223> n denotes a, g, c, or t

<400> 24
gctctagagt ydatngcncc rtartc

26

<210> 25
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> misc_feature
<222> (6)..(6)
<223> Xaa denotes Glu or Lys

<400> 25

Asp Tyr Gly Ala Ile Xaa
1 5

<210> 26
<211> 143
<212> DNA
<213> Bacillus

<400> 26
gcgtctatga cacggcaagc cgatcattcg cggaaccgc caccgtttcc ccgggacgaa 60
acggttcagc ttaccottac ggatctgtta catcgaccgc ctatttcac ccgtcgggtt 120
ggcagagcgg aaattccaat tat 143

<210> 27
<211> 48
<212> PRT

<213> Bacillus

<400> 27

Cys Val Tyr Asp Thr Ala Ser Arg Ser Phe Ala Gly Thr Ala Thr Val
1 5 10 15

Ser Pro Gly Arg Asn Gly Ser Ala Tyr Pro Tyr Gly Ser Val Thr Ser
20 25 30

Thr Arg Tyr Phe Ile Pro Ser Gly Trp Gln Ser Gly Asn Ser Asn Tyr
35 40 45

<210> 28

<211> 184

<212> DNA

<213> Bacillus

<400> 28

gatcgagctc agccagccga tcggcaatac cgctcggatat ttcgggatatt catacaccgc 60
ttcatcgctt gcaggagcag gcgtgacat cagcggatat ccaggagaca aaacaacagg 120
caccagtgg caaatgtccg gaacgatcgc tgtttcagaa acgtataaac tgcaatatgc 180
gatc 184

<210> 29

<211> 61

<212> PRT

<213> Bacillus

<400> 29

Ile Glu Leu Ser Gln Pro Ile Gly Asn Thr Val Gly Tyr Phe Gly Tyr
1 5 10 15

Ser Tyr Thr Ala Ser Ser Leu Ala Gly Ala Gly Val Thr Ile Ser Gly
20 25 30

Tyr Pro Gly Asp Lys Thr Thr Gly Thr Gln Trp Gln Met Ser Gly Thr
35 40 45

Ile Ala Val Ser Glu Thr Tyr Lys Leu Gln Tyr Ala Ile
50 55 60

<210> 30

<211> 143

<212> DNA

<213> Bacillus

<400> 30

gcatttatga cacagcgagc gggtcattcg ccggaaccgc taccgtttct ccgggacgga 60

acggttcaac atatccgtac ggatcagtta catcaaccgc ctatttcac ccgtcaggct 120
atcgaagcgg aaattcgaat tac 143

<210> 31
<211> 48
<212> PRT
<213> Bacillus

<400> 31

Cys Ile Tyr Asp Thr Ala Ser Gly Ser Phe Ala Gly Thr Ala Thr Val
1 5 10 15

Ser Pro Gly Arg Asn Gly Ser Thr Tyr Pro Tyr Gly Ser Val Thr Ser
20 25 30

Thr Arg Tyr Phe Ile Pro Ser Gly Tyr Arg Ser Gly Asn Ser Asn Tyr
35 40 45

<210> 32
<211> 184
<212> DNA
<213> Bacillus

<400> 32
catagagctc agccagccga tcggcaacac cgtcgggtat ttcggatatt cctacaccac 60
ctcgtctctc gttgggtcaa gcgttaccat catcggatat ccaggcgaca aaacatcggg 120
cacccaatgg cagatgtccg gaaatatcgc cgtctcagaa acatataaac tgcaatatgc 180
gatc 184

<210> 33
<211> 61
<212> PRT
<213> Bacillus

<400> 33

Ile Glu Leu Ser Gln Pro Ile Gly Asn Thr Val Gly Tyr Phe Gly Tyr
1 5 10 15

Ser Tyr Thr Thr Ser Ser Leu Val Gly Ser Ser Val Thr Ile Ile Gly
20 25 30

Tyr Pro Gly Asp Lys Thr Ser Gly Thr Gln Trp Gln Met Ser Gly Asn
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Ile Ala Val Ser Glu Thr Tyr Lys Leu Gln Tyr Ala Ile
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Gly Xaa Pro Xaa Asp Lys Thr

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5

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Val Val Ile Gly Gly Asp Asp Gly
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